

# SEQUENCE LISTING

<110> Braun, Jonathan  
Sutton, Christopher L.

<120> IBD-Associated Microbial Nucleic Acid  
Molecules

<130> P-PM 4966

<150> US 09/303,120

<151> 1999-04-30

<150> US 09/820,576

<151> 2001-03-28

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 302

<212> DNA

<213> Unknown

<220>

<223> Microbial Organism from the human gut

<221> CDS

<222> (2)...(301)

<400> 1  
a gat ctg gcc agc gcc gtg ggc atc cag tcc ggc agc atc ttt cat cac 49  
Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His  
1 5 10 15

ttc aag agc aag gat gag ata ttg cgt gcc gtg atg gag gaa acc atc 97  
Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile  
8 20 25 30

cat tac aac acc gcg atg atg cgc gct tca ctg gag gag gcg agc acg 145  
His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr  
35 40 45

gtg cgc gaa cgc gtg ctg gcg ctg atc cgc tgc gag ttg cag tgc atc 193  
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile  
50 55 60

atg ggc ggc agt ggc gag gcc atg ggc gtg ctg gtc tac gaa tgg cgc 241  
Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg  
65 70 75 80

↑

09966608.092701

tcg ctg tgc gcc gaa ggc cag gcg cac gtg ctg gcc ctg cgt gac gtg 289  
 Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val  
 85 90 95

tat gag cag atc t 302  
 Tyr Glu Gln Ile  
 100

<210> 2  
 <211> 100  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Microbial organism from the human gut

<400> 2  
 Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His  
 1 5 10 15  
 Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile  
 20 25 30  
 His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr  
 35 40 45  
 Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile  
 50 55 60  
 Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg  
 65 70 75 80  
 Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val  
 85 90 95  
 Tyr Glu Gln Ile  
 100

<210> 3  
 <211> 392  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Microbial Organism from the human gut

<221> CDS  
 <222> (2)...(346)

<221> misc\_feature  
 <222> (1)...(392)  
 <223> n = A,T,C or G

<400> 3  
 a gat ctt gag cgt cat gag tgc ctg ggg tac gcc ttt tca tgc cgt ccg 49  
 Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro  
 1 5 10 15

T04260-8099660

gcg gat cga gag tgg gtg ttt ttt cag ggc acg gtt tcc tac aag gta 97  
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val  
20 25 30

cga gtg gcc agc cgt ttg ctc atc aat gaa agc cgg gca ttg atg tcg 145  
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser  
35 40 45

gcg gca ttg gat ggt ttt ggc ata gtg ctc ggc ccg caa gac ttc ctg 193  
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu  
50 55 60

cga acg gcg ttg gcg agt ggc gag ttg gtg cgg gtg ttg ccg gag ttt 241  
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe  
65 70 75 80

gag gct ccg agt cgg tcg atg cat ttg gtc tac acc gca aac cgc cag 289  
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln  
85 90 95

cgt acc gcc aag ttg cgc tgc ttt gtc gag act gtg ctg gga cgt ttt 337  
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe  
100 105 110

ggt ccg gta tgaaggagca ccaccgtggc ggtcgccggg angcacctaa 386  
Gly Pro Val  
115

agatct 392

<210> 4  
<211> 115  
<212> PRT  
<213> Unknown

<220>  
<223> Microbial organism from the human gut

<400> 4  
Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro  
1 5 10 15  
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val  
20 25 30  
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser  
35 40 45  
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu  
50 55 60  
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe  
65 70 75 80  
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln  
85 90 95  
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe

0996608-092701

Gly Pro Val 100 105 110  
115

<210> 5  
<211> 114  
<212> PRT  
<213> Unknown

<220>  
<223> Microbial Organism from the human gut

<221> VARIANT  
<222> (1)...(114)  
<223> Xaa = Any Amino Acid

<400> 5  
Arg Thr Arg Arg Ile Ser Leu Pro His Lys Lys Leu Ala Arg Asn Gly  
1 5 10 15  
Val Leu Tyr Ser His Gly Ala Thr Gln Glu Asp Ile Phe Ala Pro Cys  
20 25 30  
Gln His Arg Arg Cys Gln Ile Thr Lys Ala Tyr His Glu Ala Arg Leu  
35 40 45  
Val Glu Gln Ser Arg Arg Gln Arg Thr Ala Leu Gln His Pro His Gln  
50 55 60  
Arg Leu Lys Leu Ser Arg Thr Pro Arg His Met Gln Asp Val Gly Cys  
65 70 75 80  
Val Ala Leu Thr Gly Gly Leu Gln Ala Ala Lys Asp Leu Ser His Gln  
85 90 95  
Ser Thr Lys Thr Arg Tyr Ser Pro Ala Gly Gly His Arg Asp Gly Pro  
100 105 110  
Xaa Val

<210> 6  
<211> 190  
<212> PRT  
<213> Clostridium pasteurianum

<400> 6  
Met Asn Lys Thr Lys Asp Asn Ile Phe Tyr Ser Ala Ile Lys Val Phe  
1 5 10 15  
Ser Asn Asn Gly Tyr Asn Gly Ala Thr Met Asp Glu Ile Ala Ser Asn  
20 25 30  
Ala Gly Val Ala Lys Gly Thr Leu Tyr Tyr His Phe Lys Ser Lys Glu  
35 40 45  
Glu Ile Phe Lys Tyr Ile Ile Glu Glu Gly Val Asn Leu Met Lys Asn  
50 55 60  
Glu Ile Asp Glu Ala Thr Asp Lys Glu Lys Thr Ala Leu Glu Lys Leu  
65 70 75 80  
Lys Ala Val Cys Arg Val Gln Leu Asn Leu Ile Tyr Lys Asn Arg Asp

0996603-05701

```
<210> 7
<211> 200
<212> PRT
<213> Mycobacterium tuberculosis
```

```
<210> 8
<211> 192
<212> PRT
<213> Auifex aeolicus
```

Met	Tyr	Ile	Leu	Leu	Phe	Met	Gly	Glu	Lys	Arg	Ser	Asp	Thr	Lys	Glu
1				5					10					15	
Lys	Ile	Leu	Ser	Ser	Ala	Leu	Lys	Leu	Phe	Ser	Lys	Lys	Gly	Phe	Lys
			20					25					30		
Glu	Thr	Thr	Ile	Lys	Asp	Ile	Ala	Lys	Glu	Val	Gly	Ile	Thr	Glu	Gly
		35					40					45			
Ala	Ile	Tyr	Arg	His	Phe	Thr	Ser	Lys	Glu	Glu	Ile	Ile	Lys	Ser	Leu
	50					55					60				
Leu	Glu	Ser	Ile	Thr	Lys	Glu	Leu	Arg	His	Lys	Leu	Glu	Val	Ala	Leu
65				70					75					80	
Gln	Arg	Gly	Glu	Thr	Asp	Glu	Glu	Ile	Leu	Glu	Ser	Ile	Val	Asp	Thr
			85					90					95		
Leu	Ile	Asp	Tyr	Ala	Phe	Ser	Asn	Pro	Glu	Ser	Phe	Arg	Phe	Leu	Asn
		100						105				110			
Leu	Tyr	His	Leu	Leu	Lys	Glu	Tyr	Gly	Glu	Val	Lys	Asn	Leu	Pro	Gly
	115					120					125				
Glu	Leu	Ile	Leu	Lys	Phe	Leu	Asn	Gly	Leu	Tyr	Leu	Lys	Arg	Lys	Leu
	130					135				140					
Lys	Thr	Tyr	Pro	Glu	Ile	Ala	Leu	Ala	Val	Val	Thr	Gly	Ser	Val	Glu
145				150					155					160	
Arg	Val	Phe	Ile	Phe	Lys	Glu	Arg	Asn	Phe	Leu	Asp	Tyr	Asp	Glu	Glu
			165					170					175		
Thr	Ile	Lys	Lys	Glu	Leu	Lys	Lys	Val	Leu	Lys	Ser	Ala	Ile	Leu	Ala
		180						185				190			

<213> Unknown

<223> Microbial Organism from the human gut

ccgtgggcat ccagtccg

18

<213> Unknown

<223> Microbial Organism from the human gut

tctgctcata cacgtcacg

19